

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lal, Preeti
Hillman, Jennifer L.
Guegler, Karl J.
Corley, Neil C.
Baughn, Mariah R.
Azimzai, Yalda

(ii) TITLE OF THE INVENTION: HUMAN UBIQUITIN-CONJUGATING ENZYME
HOMOLOGS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: HERewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cerrone, Michael C
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0502 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSNOT14
(B) CLONE: 1728211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met Ala Leu Leu Ala Thr Ser Leu Pro Glu Gly Ile Met Val Lys
5 10 15

Thr	Phe	Glu	Asp	Arg	Met	Asp	Leu	Phe	Ser	Ala	Leu	Ile	Lys	Gly	
				20					25					30	
Pro	Thr	Arg	Thr	Pro	Tyr	Glu	Asp	Gly	Leu	Tyr	Leu	Phe	Asp	Ile	
				35					40					45	
Gln	Leu	Pro	Asn	Ile	Tyr	Pro	Ala	Val	Pro	Pro	His	Phe	Cys	Tyr	
				50					55					60	
Leu	Ser	Gln	Cys	Ser	Gly	Arg	Leu	Asn	Pro	Asn	Leu	Tyr	Asp	Asn	
				65					70					75	
Gly	Lys	Val	Cys	Val	Ser	Leu	Leu	Gly	Thr	Trp	Ile	Gly	Lys	Gly	
				80					85					90	
Thr	Glu	Arg	Trp	Thr	Ser	Lys	Ser	Ser	Leu	Leu	Gln	Val	Leu	Ile	
				95					100					105	
Ser	Ile	Gln	Gly	Leu	Ile	Leu	Val	Asn	Glu	Pro	Tyr	Tyr	Asn	Glu	
				110					115					120	
Ala	Gly	Phe	Asp	Ser	Asp	Arg	Gly	Leu	Gln	Glu	Gly	Tyr	Glu	Asn	
				125					130					135	
Ser	Arg	Cys	Tyr	Asn	Glu	Met	Ala	Leu	Ile	Arg	Val	Val	Gln	Ser	
				140					145					150	
Met	Thr	Gln	Leu	Val	Arg	Arg	Pro	Pro	Glu	Val	Phe	Glu	Gln	Glu	
				155					160					165	
Ile	Arg	Gln	His	Phe	Ser	Thr	Gly	Gly	Trp	Arg	Leu	Val	Asn	Arg	
				170					175					180	
Ile	Glu	Ser	Trp	Leu	Glu	Thr	His	Ala	Leu	Leu	Glu	Lys	Ala	Gln	
				185					190					195	
Ala	Leu	Pro	Asn	Gly	Val	Pro	Lys	Ala	Ser	Ser	Ser	Pro	Glu	Pro	
				200					205					210	
Pro	Ala	Val	Ala	Glu	Leu	Ser	Asp	Ser	Gly	Gln	Gln	Glu	Pro	Glu	
				215					220					225	
Asp	Gly	Gly	Pro	Ala	Pro	Gly	Glu	Ala	Ser	Gln	Gly	Ser	Asp	Ser	
				230					235					240	
Glu	Gly	Gly	Ala	Gln	Gly	Leu	Ala	Phe	Ser						
				245					250						

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: SINTNOT13
 - (B) CLONE: 1803905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Ala	Gln	Gln	Gln	Met	Thr	Ser	Ser	Gln	Lys	Ala	Leu	Met	Leu	
				5					10					15	
Glu	Leu	Lys	Ser	Leu	Gln	Glu	Glu	Pro	Val	Glu	Gly	Phe	Arg	Ile	
				20					25					30	
Thr	Leu	Val	Asp	Glu	Ser	Asp	Leu	Tyr	Asn	Trp	Glu	Val	Ala	Ile	
				35					40					45	
Phe	Gly	Leu	Pro	Asn	Thr	Leu	Tyr	Glu	Gly	Gly	Tyr	Phe	Lys	Ala	
				50					55					60	
His	Ile	Lys	Phe	Pro	Ile	Asp	Tyr	Pro	Tyr	Ser	Pro	Pro	Thr	Phe	
				65					70					75	
Arg	Phe	Leu	Thr	Lys	Met	Trp	His	Pro	Asn	Ile	Tyr	Glu	Asn	Gly	
				80					85					90	
Asp	Val	Cys	Ile	Ser	Ile	Leu	His	Pro	Pro	Val	Asp	Asp	Pro	Gln	
				95					100					105	
Ser	Gly	Glu	Leu	Pro	Ser	Glu	Arg	Trp	Asn	Pro	Thr	Gln	Asn	Val	
				110					115					120	

Arg	Thr	Ile	Leu	Leu	Ser	Val	Ile	Ser	Leu	Leu	Asn	Glu	Pro	Asn	
			125						130					135	
Thr	Phe	Ser	Pro	Ala	Asn	Val	Asp	Ala	Ser	Val	Met	Phe	Arg	Lys	
			140						145					150	
Trp	Arg	Asp	Ser	Lys	Gly	Lys	Asp	Lys	Glu	Tyr	Ala	Glu	Ile	Ile	
			155						160					165	
Arg	Lys	Gln	Val	Ser	Ala	Thr	Lys	Ala	Glu	Ala	Glu	Lys	Asp	Gly	
			170						175					180	
Val	Lys	Val	Pro	Thr	Thr	Leu	Ala	Glu	Tyr	Cys	Ile	Lys	Thr	Lys	
			185						190					195	
Val	Pro	Ser	Asn	Asp	Asn	Ser	Ser	Asp	Leu	Leu	Tyr	Asp	Asp	Leu	
			200						205					210	
Tyr	Asp	Asp	Asp	Ile	Asp	Asp	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Ala	
			215						220					225	
Asp	Cys	Tyr	Asp	Asp	Asp	Asp	Ser	Gly	Met	Arg	Ser	Arg	Asp	Val	
			230						235					240	
Leu	Leu	Gln	Cys	Pro	Cys	Thr	Ala	Leu	Pro	Ser	Gln	Ala	Lys	Gly	
			245						250					255	
Arg	Gly	Ala	Ser	Gly	Asp	Leu	Ala	Met	Ala	Pro	Gln	Gln	Lys	Pro	
			260						265					270	
Ile	His	Ser	Gly	Trp	Gly	Asn	Thr	His	Ser	Ser	Cys				
			275						280						

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNTUT16
- (B) CLONE: 2792472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

Met	Glu	Thr	Arg	Tyr	Asn	Leu	Lys	Ser	Pro	Ala	Val	Lys	Arg	Leu	
				5					10					15	
Met	Lys	Glu	Ala	Ala	Glu	Leu	Lys	Asp	Pro	Thr	Asp	His	Tyr	His	
				20					25					30	
Ala	Gln	Pro	Leu	Glu	Asp	Asn	Leu	Phe	Glu	Trp	His	Phe	Thr	Val	
				35					40					45	
Arg	Gly	Pro	Pro	Asp	Ser	Asp	Phe	Asp	Gly	Gly	Val	Tyr	His	Gly	
				50					55					60	
Arg	Ile	Val	Leu	Pro	Pro	Glu	Tyr	Pro	Met	Lys	Pro	Pro	Ser	Ile	
				65					70					75	
Ile	Leu	Leu	Thr	Ala	Asn	Gly	Arg	Phe	Glu	Val	Gly	Lys	Lys	Ile	
				80					85					90	
Cys	Leu	Ser	Ile	Ser	Gly	His	His	Pro	Glu	Thr	Trp	Gln	Pro	Ser	
				95					100					105	
Trp	Ser	Ile	Arg	Thr	Ala	Leu	Leu	Ala	Ile	Ile	Gly	Phe	Met	Pro	
				110					115					120	
Thr	Lys	Gly	Glu	Gly	Ala	Ile	Gly	Ser	Leu	Asp	Tyr	Thr	Pro	Glu	
				125					130					135	
Glu	Arg	Arg	Ala	Leu	Ala	Lys	Lys	Ser	Gln	Asp	Phe	Cys	Cys	Glu	
				140					145					150	
Gly	Cys	Gly	Ser	Ala	Met	Lys	Asp	Val	Leu	Leu	Pro	Leu	Lys	Ser	
				155					160					165	
Gly	Ser	Asp	Ser	Ser	Gln	Ala	Asp	Gln	Glu	Ala	Lys	Glu	Leu	Ala	
				170					175					180	
Arg	Gln	Ile	Ser	Phe	Lys	Ala	Glu	Val	Asn	Ser	Ser	Gly	Lys	Thr	
				185					190					195	

Ile	Ser	Glu	Ser	Asp	Leu	Asn	His	Ser	Phe	Ser	Leu	Thr	Asp	Leu
				200					205					210
Gln	Asp	Asp	Ile	Pro	Thr	Thr	Phe	Gln	Gly	Ala	Thr	Ala	Ser	Thr
				215					220					225
Ser	Tyr	Gly	Leu	Gln	Asn	Ser	Ser	Ala	Ala	Ser	Phe	His	Gln	Pro
				230					235					240
Thr	Gln	Pro	Val	Ala	Lys	Asn	Thr	Ser	Met	Ser	Pro	Arg	Gln	Arg
				245					250					255
Arg	Ala	Gln	Gln	Gln	Ser	Gln	Arg	Arg	Leu	Ser	Thr	Ser	Pro	Asp
				260					265					270
Val	Ile	Gln	Gly	His	Gln	Pro	Arg	Asp	Asn	His	Thr	Asp	His	Gly
				275					280					285
Gly	Ser	Ala	Val	Leu	Ile	Val	Ile	Leu	Thr	Leu	Ala	Leu	Ala	Ala
				290					295					300
Leu	Ile	Phe	Arg	Arg	Ile	Tyr	Leu	Ala	Asn	Glu	Tyr	Ile	Phe	Asp
				305					310					315
Phe	Glu	Leu												

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1006 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: PROSNOT14
 (B) CLONE: 1728211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

AGGTCPTCTC	CGTACTGGAG	TTTGACCCCT	CAAATCATTC	TTTAAAGAA	ATTGAGTTCC	60
AGCCTCCAGA	AGCCAAGAAG	TTCTTCAGCA	CAGTGC GGAA	GGAGATGGCG	CTGCTGGCTA	120
CCTCACTGCC	TGAGGGCATC	ATGGTCAAGA	CTTTTGAAGA	TAGAATGGAC	CTCTCTCAGC	180
CTCTCATCAA	GGGCCCACT	CGAACCCCT	ACGAGGATGG	CCTCTACTTG	TTTGACATCC	240
AGCTCCCAA	CATCTACCCA	GCCGTGCC	CCCACTCTG	CTACCTCTCC	CAATGCAGTG	300
GCGCCTGAA	CCCCAACCTG	TATGACAATG	GGAAGGTGTG	TGTCAGCCTC	CTGGGCACCT	360
GGATTGGA	GGGACAGAG	AGGTGGACAA	GCAAGTCCAG	CCTTCTCCAG	GTGCTCATCT	420
CCATCCAAG	TCTGATCTG	GTAATGAAC	CATACTACAA	CGAAGCCGGC	TTGCAGAGTG	480
ACCGAGGCT	CGAGGAAGGC	TATGAAACAA	GTCTGTGTTA	CAATGAGATG	GCGCTGATCC	540
GCGTGGTGA	GTCCATGACC	CAGCTGGTGC	GCGGCCCCC	CGAGGTCTTT	GAGCAGGAGA	600
TCAGGCAACA	CTTTAGCACT	GGTGGTGGC	GGCTGGTGAA	CCGTATCGAG	TCCTGGCTGG	660
AAACCCATGC	CCTGCTGGAG	AAGGCCCAGG	CACTGCCCAA	CGGGTGCC	AAGGCCAGCA	720
GCTCGCCACA	GCCCCAGCT	GTAGCCGAGC	TGTGAGACTC	CGGCCAACAA	GAACCTGAGG	780
ATGAGGCGCC	AGCCCCAGGA	GAGGCTTCCC	AGGGCTCAGA	CTCAGAGGGC	GGTGCCCAGG	840
GCTTGCCCTT	CAGCTAGCAG	GGACCAACA	GACCAGACTT	CGGAGACCCG	ACCAAGCCGA	900
TCGGTGCCAC	CCAGTGTGAA	ACCCAAAGAA	GCGGAGAAAG	AGCNTTAAGA	GCTACCCGAG	960
CTTCTTACCT	GAGAAGAGTG	GCTACCCTGA	CATCGGCTTC	CCCCTC		1006

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2067 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: SINTNOT13
 (B) CLONE: 1803905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

TTTTNTGTGT	GTGNCNCCNG	TNMGTNCCCC	TNCTANGTGG	TGGGNTTGT	TGNTNGGTGC	60
TTCTCTGTGT	TNTNTTNNCC	TTGCCATGTC	CTCAGNCTTC	CNTCTCNTNT	NNNCNNTTPT	120
TGNCNCNCCC	CNATATGCN	TGCGCCCTAG	NMGTTCGNMN	CNCCCCAAA	GNCTCTNGNC	140
TNCTNCTGAA	AGGNNCCCC	CTNNGAAAAG	GCCTNCTCGG	NAATTTGNGT	AAAAAATACC	180
CCCNNTGCCA	AGGGNGGNG	GGGAAAAACC	CGGGTTNGG	AAAGGGGGCN	TTTTNCCNGC	240
GNNTTNNCCC	CCCTCTTGG	GTNTGNNACC	GNMTTCCCC	NGANCTTNT	TTAACNAANC	300
TTGGGGGAAG	GTNTNNCCAA	NTNTTTTCGG	GACTTCCCC	CAACACNCT	TTTANNGGAA	420
NGGCGGNCNT	ATTTCCTCGG	CCGAGGGTTA	CATTCTGATG	TTGGAGCGCC	GCCCGCGCGA	480
TGGCCAGCA	GCGATGACG	AGCTCGCAGA	AGGCCCTGAT	GCTCGAGCTG	AAATCTCTGC	540
AGGAGGAACC	GCTGGAGGGC	TTCCGGATCA	CCCTTGTGGA	CGAGTCCGAC	CTCTACAAC	600
GGGAGGTGG	CATCTTCGGA	TCCCCAACCA	CCCTCTACGA	AGCGGCTAC	TTCAAGCGCC	660
ATATTAATTT	TCCTATTGAC	TACCCCTATT	CACCACCTAC	CTTCAGATT	TTGACAAAA	720
TGTGGCACCC	CAACATTAT	GAGATGGAG	ATGTATGCAT	TTTGATTCTT	CATCCGCTTG	780
TAGATGACCC	ACAGAGTGG	GAATTCGCTT	CTGAAAGGTG	GAATCCTACT	CAGAAATGTA	840
GGCATCTCT	ATTAACTGTA	ATCTCACTCG	TAAATGAGCC	CAACACCTTC	TCCCCAGCCA	900
ATGTGATGCT	TTGAGTTATG	TTCAAGAAAT	GGAGAGACAG	TAAAGGAAAA	GACAAAGAA	960
ATGCTGAAT	TATTAGGAAA	CAAGTTTCAG	CCACTAAGGC	CGAAGCAGAA	AAGGATGGAG	1020
TGAAGTCCC	CACAACCTG	GCGGAATACT	GCATCAAAAC	TAAAGTGCTT	TCCCAATGACA	1080
ACAGCTCAGA	TTTGCTTTAC	GACGACTTGT	ATGATGACGA	CATTGTGATG	GAAGATGAGG	1140
AGGAGGAAGA	TGCCGACTGT	TATGATGATG	ATGATTCTGG	GATGAGGAGT	CGTGACGTGC	1200
TCCTTCACTG	CCCTGTACT	GCCCTGCCAT	CTCAGGCCAA	AGGAGGGGGA	GCAAGTGGGG	1260
ACCTGGCCAT	GGCCCCCTAG	CAAAAACTTA	TTCAACAGCG	GTGGGGAAAC	ACACACAGCT	1320
CCTGCTGACT	CCCTCTATGG	ATCTCAGTTT	GCTCCTTTT	ATGGACCTTT	AATGGAGAGA	1380
GAGTAACCTT	CCACAGAATG	TCTGAATCTT	TGCATTCTTT	ACCTTCCAT	CACATATTG	1440
ATTCTTTTTT	TAAAAAATAT	GAACCCAAAC	TCCCGCTTCA	CTTCGATCT	CAGGAATGTT	1500
CACAGCAAAA	CACGTTTGGT	CTGTTTTTAG	ATTCTTGAAG	AATCTCAATG	TCTTTCAAGA	1560
GTTTTAATGT	GTTTAAAGCT	GGGAACCTGT	TGGGAGTTCA	CAATGTCTGC	ATATACCTGG	1620
TAGCAAAAGA	AAATGGAAAA	AAACCCACAA	AACAACATTT	AAAAAATAAA	AAAAACAAT	1680
TGCAAGCTG	TTAGCTGCTC	ATTTACATTA	GTGTGTGTGC	ATTCGTTGAC	CCCCATGGTG	1740
GTGAATCTGT	TTTCTTCTCT	TTCTTAAGGC	TGGGACATGG	TGGGCATCAG	GGACCTTTGT	1800
CTAAGCTGCA	TGAATGTGTC	TCCTTCAATC	TCCATGAAC	TGAGCTAACA	TGGAGCGCTC	1860
AGCTGTCTGT	AGGAGAGAAA	TCAGACTTTT	TTTTTTGAAT	TGAGTTGGGA	TCGAAAGCCT	1920
GAATAAATA	TTCACTACTT	CCATAGTCCA	CCCAAAATGA	AAAGGAGGAA	GAAAAAATAA	1980
AAGGGGGGGG	GCGCCGCCTA	GTGACCCCTG	TCGACCCGGG	AATTAATTC	CGGACCGGGA	2040
CCTGCAGGG	TGTACCAGGT	TTTCCCT				2067

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1067 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNUT16
- (B) CLONE: 2792472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

cgggagggcg	gagccaagcc	agcgaccac	catggagacc	cgctacaacc	tgaagagtc	60
gggtgttaaa	cgtttaata	aagaagggc	agaattgaaa	gatccaacag	atcattacca	120
tggcgagcct	tttaggagta	acctttttga	atggcacttc	acggttagag	ggccccacca	180
cctccgtttt	gatggagag	tttatcacgg	gcggatagta	ctgcaccagc	agatcccat	240
gaaccaccca	agcattatc	tctaacggc	taattggtcga	tttgaagtgg	gcaagaaaa	300
ctgttttgag	atccagccc	atcatcctga	aacttggcag	cctctgtgga	gtataaagac	360
agcattatta	cctcatcttg	ggtttatgcc	aacaaaaagg	gagggagcca	taggttctct	420
agttacactc	gcagagaaa	gaagagcact	tgccccaaaa	tcacaaagt	tctgttgtga	480
aggatgtggc	tctgcatcga	aggatgtcct	gttgctctta	aaactctggg	gcgattcaag	540
ccaagctggc	caagaagcca	aagaactggc	taggcaataa	agcttttgga	cgaaagtcca	600
ttcatctgga	aagactatct	ctgagtcaga	cttaaacacc	tctttttcac	taactgatt	660
acaagatgat	agactacaaa	cattccagg	tgcatcgcc	agtcactcgt	acggactcca	720
gaattctcta	gcagcatcct	ttcatcaacc	taccacacct	gtagctaaga	atactccat	780

PF-0502-1 DIV

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tgtaatccag ggccaccagc caagagacaa ccacactgat catgggtgggt cagctgtact 900
gattgtcatc ctgacttttg cattggcagc tcttatattc cgacgaatat atctgggcaa 960
cgaatacata tttgactttg agttataata tggttttgtg acttatgagc tgtgactcaa 1020
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